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SEQUENCE LISTING

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LESAGE, FLORIAN
ROMEY, GEORGES

<120> HUMAN TREK2, A STRETCH-AND ARACHIDONIC ACID-SENSITIVE
K+ CHANNEL ACTIVATED BY INHALATIONAL ANESTHETICS AND
RILUZOLE

<130> 1256-R-00

<140> 09/892,360

<141> 2001-06-27

<150> 60/214,559

<151> 2000-06-27

<160> 25

<170> PatentIn Ver. 2.1

<210> 1

<211> 1614

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1614)

<223> ORF of human TREK2 cDNA

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gca	gca	gca	ccg	gtg	tgc	cag	ccc	aag	agc	gcc	act	aac	ggg	caa	ccc	96
Ala	Ala	Ala	Pro	Val	Cys	Gln	Pro	Lys	Ser	Ala	Thr	Asn	Gly	Gln	Pro	
			20					25					30			

ccg	gct	ccg	gct	ccg	act	cca	act	ccg	cgc	ctg	tcc	att	tcc	tcc	cga	144
Pro	Ala	Pro	Ala	Pro	Thr	Pro	Thr	Pro	Arg	Leu	Ser	Ile	Ser	Ser	Arg	
		35					40					45				

gcc	aca	gtg	gta	gcc	agg	atg	gaa	ggc	acc	tcc	caa	ggg	ggc	ttg	cag	192
Ala	Thr	Val	Val	Ala	Arg	Met	Glu	Gly	Thr	Ser	Gln	Gly	Gly	Leu	Gln	
	50					55					60					

acc	gtc	atg	aag	tgg	aag	acg	gtg	gtt	gcc	atc	ttt	gtg	gtt	gtg	gtg	240
Thr	Val	Met	Lys	Trp	Lys	Thr	Val	Val	Ala	Ile	Phe	Val	Val	Val	Val	
65					70				75					80		

gtc	tac	ctt	gtc	act	ggc	ggc	ctt	gtc	ttc	cgg	gca	ttg	gag	cag	ccc	288
Val	Tyr	Leu	Val	Thr	Gly	Gly	Leu	Val	Phe	Arg	Ala	Leu	Glu	Gln	Pro	
			85					90						95		

ttt gag agc agc cag aag aat acc atc gcc ttg gag aag gcg gaa ttc	336
Phe Glu Ser Ser Gln Lys Asn Thr Ile Ala Leu Glu Lys Ala Glu Phe	
100 105 110	
ctg cgg gat cat gtc tgt gtg agc ccc cag gag ctg gag acg ttg atc	384
Leu Arg Asp His Val Cys Val Ser Pro Gln Glu Leu Glu Thr Leu Ile	
115 120 125	
cag cat gct ctt gat gct gac aat gcg gga gtc agt cca ata gga aac	432
Gln His Ala Leu Asp Ala Asp Asn Ala Gly Val Ser Pro Ile Gly Asn	
130 135 140	
tct tcc aac aac agc agc cac tgg gac ctc ggc agt gcc ttt ttc ttt	480
Ser Ser Asn Asn Ser Ser His Trp Asp Leu Gly Ser Ala Phe Phe Phe	
145 150 155 160	
gct gga act gtc att acg acc ata ggg tat ggg aat att gct ccg agc	528
Ala Gly Thr Val Ile Thr Thr Ile Gly Tyr Gly Asn Ile Ala Pro Ser	
165 170 175	
act gaa gga ggc aaa atc ttt tgt att tta tat gcc atc ttt gga att	576
Thr Glu Gly Gly Lys Ile Phe Cys Ile Leu Tyr Ala Ile Phe Gly Ile	
180 185 190	
cca ctc ttt ggt ttc tta ttg gct gga att gga gac caa ctt gga acc	624
Pro Leu Phe Gly Phe Leu Leu Ala Gly Ile Gly Asp Gln Leu Gly Thr	
195 200 205	
atc ttt ggg aaa agc att gca aga gtg gag aag gtc ttt cga aaa aag	672
Ile Phe Gly Lys Ser Ile Ala Arg Val Glu Lys Val Phe Arg Lys Lys	
210 215 220	
caa gtg agt cag acc aag atc cgg gtc atc tca acc atc ctg ttc atc	720
Gln Val Ser Gln Thr Lys Ile Arg Val Ile Ser Thr Ile Leu Phe Ile	
225 230 235 240	
ttg gcc ggc tgc att gtg ttt gtg acg atc cct gct gtc atc ttt aag	768
Leu Ala Gly Cys Ile Val Phe Val Thr Ile Pro Ala Val Ile Phe Lys	
245 250 255	
tac atc gag ggc tgg acg gcc ttg gag tcc att tac ttt gtg gtg gtc	816
Tyr Ile Glu Gly Trp Thr Ala Leu Glu Ser Ile Tyr Phe Val Val Val	
260 265 270	
act ctg acc acg gtg ggc ttt ggt gat ttt gtg gca ggg gga aac gct	864
Thr Leu Thr Thr Val Gly Phe Gly Asp Phe Val Ala Gly Gly Asn Ala	
275 280 285	
ggc atc aat tat cgg gag tgg tat aag ccc cta gtg tgg ttt tgg atc	912
Gly Ile Asn Tyr Arg Glu Trp Tyr Lys Pro Leu Val Trp Phe Trp Ile	
290 295 300	
ctt gtt ggc ctt gcc tac ttt gca gct gtc ctc agt atg atc gga gat	960
Leu Val Gly Leu Ala Tyr Phe Ala Ala Val Leu Ser Met Ile Gly Asp	
305 310 315 320	

tgg cta cgg gtt ctg tcc aaa aag aca aaa gaa gag gtg ggt gaa atc	1008
Trp Leu Arg Val Leu Ser Lys Lys Thr Lys Glu Glu Val Gly Glu Ile	
325 330 335	
aag gcc cat gcg gca gag tgg aag gcc aat gtc acg gct gag ttc cgg	1056
Lys Ala His Ala Ala Glu Trp Lys Ala Asn Val Thr Ala Glu Phe Arg	
340 345 350	
gag aca cgg cga agg ctc agc gtg gag atc cac gat aag ctg cag cgg	1104
Glu Thr Arg Arg Arg Leu Ser Val Glu Ile His Asp Lys Leu Gln Arg	
355 360 365	
gcg gcc acc atc cgc agc atg gag cgc cgg cgg ctg ggc ctg gac cag	1152
Ala Ala Thr Ile Arg Ser Met Glu Arg Arg Arg Leu Gly Leu Asp Gln	
370 375 380	
cgg gcc cac tca ctg gac atg ctg tcc ccc gag aag cgc tct gtc ttt	1200
Arg Ala His Ser Leu Asp Met Leu Ser Pro Glu Lys Arg Ser Val Phe	
385 390 395 400	
gct gcc ctg gac acc ggc cgc ttc aag gcc tca tcc cag gag agc atc	1248
Ala Ala Leu Asp Thr Gly Arg Phe Lys Ala Ser Ser Gln Glu Ser Ile	
405 410 415	
aac aac cgg ccc aac aac ctg cgc ctg aag ggg ccg gag cag ctg aac	1296
Asn Asn Arg Pro Asn Asn Leu Arg Leu Lys Gly Pro Glu Gln Leu Asn	
420 425 430	
aag cat ggg cag ggt gcg tcc gag gac aac atc atc aac aag ttc ggg	1344
Lys His Gly Gln Gly Ala Ser Glu Asp Asn Ile Ile Asn Lys Phe Gly	
435 440 445	
tcc acc tcc aga ctc acc aag agg aaa aac aag gac ctc aaa aag acc	1392
Ser Thr Ser Arg Leu Thr Lys Arg Lys Asn Lys Asp Leu Lys Lys Thr	
450 455 460	
ttg ccc gag gac gtt cag aaa atc tac aag acc ttc cgg aat tac tcc	1440
Leu Pro Glu Asp Val Gln Lys Ile Tyr Lys Thr Phe Arg Asn Tyr Ser	
465 470 475 480	
ctg gac gag gag aag aaa gag gag gag acg gaa aag atg tgt aac tca	1488
Leu Asp Glu Glu Lys Lys Glu Glu Glu Thr Glu Lys Met Cys Asn Ser	
485 490 495	
gac aac tcc agc aca gcc atg ctg acg gac tgt atc cag cag cac gct	1536
Asp Asn Ser Ser Thr Ala Met Leu Thr Asp Cys Ile Gln Gln His Ala	
500 505 510	
gag ttg gag aac gga atg ata ccc acg gac acc aaa gac cgg gag ccg	1584
Glu Leu Glu Asn Gly Met Ile Pro Thr Asp Thr Lys Asp Arg Glu Pro	
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 <212> PRT
 <213> Homo sapiens

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Pro	Ala	Pro	Ala	Pro	Thr	Pro	Thr	Pro	Arg	Leu	Ser	Ile	Ser	Ser	Arg
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Ala	Thr	Val	Val	Ala	Arg	Met	Glu	Gly	Thr	Ser	Gln	Gly	Gly	Leu	Gln
	50					55					60				
Thr	Val	Met	Lys	Trp	Lys	Thr	Val	Val	Ala	Ile	Phe	Val	Val	Val	Val
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Val	Tyr	Leu	Val	Thr	Gly	Gly	Leu	Val	Phe	Arg	Ala	Leu	Glu	Gln	Pro
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Phe	Glu	Ser	Ser	Gln	Lys	Asn	Thr	Ile	Ala	Leu	Glu	Lys	Ala	Glu	Phe
			100					105					110		
Leu	Arg	Asp	His	Val	Cys	Val	Ser	Pro	Gln	Glu	Leu	Glu	Thr	Leu	Ile
		115					120				125				
Gln	His	Ala	Leu	Asp	Ala	Asp	Asn	Ala	Gly	Val	Ser	Pro	Ile	Gly	Asn
	130					135					140				
Ser	Ser	Asn	Asn	Ser	Ser	His	Trp	Asp	Leu	Gly	Ser	Ala	Phe	Phe	Phe
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Ala	Gly	Thr	Val	Ile	Thr	Thr	Ile	Gly	Tyr	Gly	Asn	Ile	Ala	Pro	Ser
				165					170					175	
Thr	Glu	Gly	Gly	Lys	Ile	Phe	Cys	Ile	Leu	Tyr	Ala	Ile	Phe	Gly	Ile
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Pro	Leu	Phe	Gly	Phe	Leu	Leu	Ala	Gly	Ile	Gly	Asp	Gln	Leu	Gly	Thr
		195					200					205			
Ile	Phe	Gly	Lys	Ser	Ile	Ala	Arg	Val	Glu	Lys	Val	Phe	Arg	Lys	Lys
	210					215					220				
Gln	Val	Ser	Gln	Thr	Lys	Ile	Arg	Val	Ile	Ser	Thr	Ile	Leu	Phe	Ile
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Leu	Ala	Gly	Cys	Ile	Val	Phe	Val	Thr	Ile	Pro	Ala	Val	Ile	Phe	Lys
				245					250					255	
Tyr	Ile	Glu	Gly	Trp	Thr	Ala	Leu	Glu	Ser	Ile	Tyr	Phe	Val	Val	Val
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Thr Leu Thr Thr Val Gly Phe Gly Asp Phe Val Ala Gly Gly Asn Ala
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 Gly Ile Asn Tyr Arg Glu Trp Tyr Lys Pro Leu Val Trp Phe Trp Ile
 290 300
 Leu Val Gly Leu Ala Tyr Phe Ala Ala Val Leu Ser Met Ile Gly Asp
 305 310 315 320
 Trp Leu Arg Val Leu Ser Lys Lys Thr Lys Glu Glu Val Gly Glu Ile
 325 330 335
 Lys Ala His Ala Ala Glu Trp Lys Ala Asn Val Thr Ala Glu Phe Arg
 340 345 350
 Glu Thr Arg Arg Arg Leu Ser Val Glu Ile His Asp Lys Leu Gln Arg
 355 360 365
 Ala Ala Thr Ile Arg Ser Met Glu Arg Arg Arg Leu Gly Leu Asp Gln
 370 375 380
 Arg Ala His Ser Leu Asp Met Leu Ser Pro Glu Lys Arg Ser Val Phe
 385 390 395 400
 Ala Ala Leu Asp Thr Gly Arg Phe Lys Ala Ser Ser Gln Glu Ser Ile
 405 410 415
 Asn Asn Arg Pro Asn Asn Leu Arg Leu Lys Gly Pro Glu Gln Leu Asn
 420 425 430
 Lys His Gly Gln Gly Ala Ser Glu Asp Asn Ile Ile Asn Lys Phe Gly
 435 440 445
 Ser Thr Ser Arg Leu Thr Lys Arg Lys Asn Lys Asp Leu Lys Lys Thr
 450 455 460
 Leu Pro Glu Asp Val Gln Lys Ile Tyr Lys Thr Phe Arg Asn Tyr Ser
 465 470 475 480
 Leu Asp Glu Glu Lys Lys Glu Glu Glu Thr Glu Lys Met Cys Asn Ser
 485 490 495
 Asp Asn Ser Ser Thr Ala Met Leu Thr Asp Cys Ile Gln Gln His Ala
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 <220>
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 <210> 5
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 <220>
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<211> 20

<212> DNA

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Val	Glu	Ser 35	Asp	Thr	Thr	Ile	Asn 40	Val	Met	Lys	Trp	Lys 45	Thr	Val	Ser
Thr	Ile 50	Phe	Leu	Val	Val	Val 55	Leu	Tyr	Leu	Ile	Ile 60	Gly	Ala	Thr	Val
Phe 65	Lys	Ala	Leu	Glu	Gln 70	Pro	His	Glu	Ile	Ser 75	Gln	Arg	Thr	Thr	Ile 80
Val	Ile	Gln	Lys	Gln 85	Thr	Phe	Ile	Ser	Gln 90	His	Ser	Cys	Val	Asn 95	Ser
Thr	Glu	Leu	Asp 100	Glu	Leu	Ile	Gln	Gln 105	Ile	Val	Ala	Ala	Ile 110	Asn	Ala
Gly	Ile	Ile 115	Pro	Leu	Gly	Asn	Thr 120	Ser	Asn	Gln	Ile	Ser 125	His	Trp	Asp
Leu 130	Gly	Ser	Ser	Phe	Phe 135	Phe	Ala	Gly	Thr	Val	Ile 140	Thr	Thr	Ile	Gly
Phe 145	Gly	Asn	Ile	Ser	Pro 150	Arg	Thr	Glu	Gly	Gly 155	Lys	Ile	Phe	Cys	Ile 160
Ile	Tyr	Ala	Leu	Leu 165	Gly	Ile	Pro	Leu	Phe 170	Gly	Phe	Leu	Leu	Ala 175	Gly
Val	Gly	Asp 180	Gln	Leu	Gly	Thr	Ile	Phe 185	Gly	Lys	Gly	Ile	Ala 190	Lys	Val
Glu	Asp 195	Thr	Phe	Ile	Lys	Trp	Asn 200	Val	Ser	Gln	Thr	Lys 205	Ile	Arg	Ile
Ile 210	Ser	Thr	Ile	Ile	Phe 215	Ile	Leu	Phe	Gly	Cys	Val 220	Leu	Phe	Val	Ala
Leu 225	Pro	Ala	Ile	Ile	Phe 230	Lys	His	Ile	Glu	Gly 235	Trp	Ser	Ala	Leu	Asp 240
Ala	Ile	Tyr	Phe	Val 245	Val	Ile	Thr	Leu	Thr 250	Thr	Ile	Gly	Phe	Gly 255	Asp
Tyr	Val	Ala	Gly 260	Gly	Ser	Asp	Ile	Glu 265	Tyr	Leu	Asp	Phe 270	Tyr	Lys	Pro

Val Val Trp Phe Trp Ile Leu Val Gly Leu Ala Tyr Phe Ala Ala Val
 275 280 285
 Leu Ser Met Ile Gly Asp Trp Leu Arg Val Ile Ser Lys Lys Thr Lys
 290 295 300
 Glu Glu Val Gly Glu Phe Arg Ala His Ala Ala Glu Trp Thr Ala Asn
 305 310 315 320
 Val Thr Ala Glu Phe Lys Glu Thr Arg Arg Arg Leu Ser Val Glu Ile
 325 330 335
 Tyr Asp Lys Phe Gln Arg Ala Thr Ser Ile Lys Arg Lys Leu Ser Ala
 340 345 350
 Glu Leu Ala Gly Asn His Asn Gln Glu Leu Thr Pro Cys Arg Arg Thr
 355 360 365
 Leu Ser Val Asn His Leu Thr Asn Glu Arg Asp Val Leu Pro Pro Leu
 370 375 380
 Leu Lys Thr Glu Ser Ile Tyr Leu Asn Gly Leu Thr Pro His Cys Ala
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 Gly Glu Glu Ile Ala Val Ile Glu Asn Ile Lys
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<210> 19

<211> 398

<212> PRT

<213> Mus musculus

<400> 19

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 35 40 45
 Asp His Pro Cys Val Ser Gln Lys Ser Leu Glu Asp Phe Ile Lys Leu
 50 55 60
 Leu Val Glu Ala Leu Gly Gly Gly Ala Asn Pro Glu Thr Ser Trp Thr
 65 70 75 80
 Asn Ser Ser Asn His Ser Ser Ala Trp Asn Leu Gly Ser Ala Phe Phe
 85 90 95
 Phe Ser Gly Thr Ile Ile Thr Thr Ile Gly Tyr Gly Asn Ile Val Leu
 100 105 110
 His Thr Asp Ala Gly Arg Leu Phe Cys Ile Phe Tyr Ala Leu Val Gly
 115 120 125

Ile Pro Leu Phe Gly Met Leu Leu Ala Gly Val Gly Asp Arg Leu Gly
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 Ser Ser Leu Arg Arg Gly Ile Gly His Ile Glu Ala Ile Phe Leu Lys
 145 150 155 160
 Trp His Val Pro Pro Gly Leu Val Arg Ser Leu Ser Ala Val Leu Phe
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 Ser Tyr Met Glu Ser Trp Ser Lys Leu Glu Ala Ile Tyr Phe Val Ile
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 Val Thr Leu Thr Thr Val Gly Phe Gly Asp Tyr Val Pro Gly Asp Gly
 210 215 220
 Thr Gly Gln Asn Ser Pro Ala Tyr Gln Pro Leu Val Trp Phe Trp Ile
 225 230 235 240
 Leu Phe Gly Leu Ala Tyr Phe Ala Ser Val Leu Thr Thr Ile Gly Asn
 245 250 255
 Trp Leu Arg Ala Val Ser Arg Arg Thr Arg Ala Glu Met Gly Gly Leu
 260 265 270
 Thr Ala Gln Ala Ala Ser Trp Thr Gly Thr Val Thr Ala Arg Val Thr
 275 280 285
 Gln Arg Thr Gly Pro Ser Ala Pro Pro Pro Glu Lys Glu Gln Pro Leu
 290 295 300
 Leu Pro Ser Ser Leu Pro Ala Pro Pro Ala Val Val Glu Pro Ala Gly
 305 310 315 320
 Arg Pro Gly Ser Pro Ala Pro Ala Glu Lys Val Glu Thr Pro Ser Pro
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 Pro Thr Ala Ser Ala Leu Asp Tyr Pro Ser Glu Asn Leu Ala Phe Ile
 340 345 350
 Asp Glu Ser Ser Asp Thr Gln Ser Glu Arg Gly Cys Ala Leu Pro Arg
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